



Additional File 7: Taxonomic composition identified using 16S sequences for all 21 samples ordered by increasing age and frailty from left to right at the phylum (A), family (B), and genus (C) levels.

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k_Bacteria; p_
  k_Bacteria; p_Acidobacteria
k_Bacteria; p_Actinobacteria
k_Bacteria; p_Armatimonadetes
k_Bacteria; p_BHI80-139
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k_Bacteria; p_ BRC1

k_Bacteria; p_Bacteroidetes k Bacteria; p Caldithrix k Bacteria; p Chlorobi

k_Bacteria; p_Chloroflexi

k Bacteria; p Cyanobacteria k_Bacteria; p_Deferribacteres

k_Bacteria; p_Elusimicrobia

k Bacteria; p FBP k Bacteria; p_Fibrobacteres

k Bacteria; p Firmicutes

k Bacteria; p Fusobacteria

k_Bacteria; p_GN04 k Bacteria; p GOUTA4

k Bacteria; p Gemmatimonadetes k Bacteria; p Hyd24-12 k _Bacteria; p__Nitrospirae

k_Bacteria; p_OP8 k Bacteria; p_Planctomycetes k Bacteria; p Proteobacteria k_Bacteria; p_SAR406

k Bacteria; p Spirochaetes k Bacteria; p Synergistetes

k_Bacteria; p_TM6 k_Bacteria; p TM7

k_Bacteria; p_TPD-58 k_Bacteria; p_Tenericutes k_Bacteria; p_Verrucomicrobia k_Bacteria; p_WPS-2

k_Bacteria; p_WS1 k_Bacteria; p_WS3 k_Bacteria; p_ZB3

k Bacteria; p [Thermi]







